

QY 61 IEREVSILRQVLAHNVITLHDVYENRTDVVHILELVSGGELFDPLAQKESISEEATSFI 120
DB 61 IEREVSILRQVLAHNVITLHDVYENRTDVVHILELVSGGELFDPLAQKESISEEATSFI 120
QY 121 KOILDGVNVLHKKTAHFDLKPENIMLLDKNIPPHIKLIDFGLAHEIDEGVEFNINIGT 180
DB 121 KOILDGVNVLHKKTAHFDLKPENIMLLDKNIPPHIKLIDFGLAHEIDEGVEFNINIGT 180
QY 181 PEFAPEIYNVEPLGLEADMSIGVITYILLSGASPLGDTKQOETLANITSVSDPDEEF 240
DB 181 PEFAPEIYNVEPLGLEADMSIGVITYILLSGASPLGDTKQOETLANITSVSDPDEEF 240
QY 241 FSHTSSELAQDFIRKLVLKETRRKLTIOEALRHPWITPVNQOAMVRBSVNLNFRKQY 300
DB 241 FSHTSSELAQDFIRKLVLKETRRKLTIOEALRHPWITPVNQOAMVRBSVNLNFRKQY 300
QY 301 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDELNRCESDTEEDIAARRKALHPRRSSTS 360
DB 301 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDELNRCESDTEEDIAARRKALHPRRSSTS 360

RESULT 2
PCT-US99-13411-2

Sequence 2, Application PC/TUS9913411A
GENERAL INFORMATION:
APPLICANT: KIMCHI, Adi
APPLICANT: MCINNIS A., Patricia
APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
FILE REFERENCE: KIMCH12A
CURRENT APPLICATION NUMBER: PCT/US99/13411A
CURRENT FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,294
EARLIER FILING DATE: 1998-06-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 360
TYPE: PRT
ORGANISM: Human
PCT-US99-13411-2

Query Match 100.0%; Score 1846; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.6e-136;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPKQKQVEDFYDIGELSGGFATVKKCKREKSTGLEVAAKFIKKRQSRASRGVSREE 60
DB 1 MEPPKQKQVEDFYDIGELSGGFATVKKCKREKSTGLEVAAKFIKKRQSRASRGVSREE 60
QY 61 IEREVSILRQVLAHNVITLHDVYENRTDVVHILELVSGGELFDPLAQKESISEEATSFI 120
DB 61 IEREVSILRQVLAHNVITLHDVYENRTDVVHILELVSGGELFDPLAQKESISEEATSFI 120
QY 121 KOILDGVNVLHKKTAHFDLKPENIMLLDKNIPPHIKLIDFGLAHEIDEGVEFNINIGT 180
DB 121 KOILDGVNVLHKKTAHFDLKPENIMLLDKNIPPHIKLIDFGLAHEIDEGVEFNINIGT 180
QY 181 PEFAPEIYNVEPLGLEADMSIGVITYILLSGASPLGDTKQOETLANITSVSDPDEEF 240
DB 181 PEFAPEIYNVEPLGLEADMSIGVITYILLSGASPLGDTKQOETLANITSVSDPDEEF 240
QY 241 FSHTSSELAQDFIRKLVLKETRRKLTIOEALRHPWITPVNQOAMVRBSVNLNFRKQY 300
DB 241 FSHTSSELAQDFIRKLVLKETRRKLTIOEALRHPWITPVNQOAMVRBSVNLNFRKQY 300
QY 301 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDELNRCESDTEEDIAARRKALHPRRSSTS 360
DB 301 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDELNRCESDTEEDIAARRKALHPRRSSTS 360

RESULT 3
US-09-719-748-2

Sequence 2, Application us/09719748

GENERAL INFORMATION:
APPLICANT: KIMCHI, Adi
TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
FILE REFERENCE: KIMCH12A
CURRENT APPLICATION NUMBER: US/09/719,748
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/089,294
PRIOR FILING DATE: 1998-06-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 360
TYPE: PRT
ORGANISM: Human
US-09-719-748-2

Query Match 100.0%; Score 1846; DB 21; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.6e-136;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPKQKQVEDFYDIGELSGGFATVKKCKREKSTGLEVAAKFIKKRQSRASRGVSREE 60
DB 1 MEPPKQKQVEDFYDIGELSGGFATVKKCKREKSTGLEVAAKFIKKRQSRASRGVSREE 60
QY 61 IEREVSILRQVLAHNVITLHDVYENRTDVVHILELVSGGELFDPLAQKESISEEATSFI 120
DB 61 IEREVSILRQVLAHNVITLHDVYENRTDVVHILELVSGGELFDPLAQKESISEEATSFI 120
QY 121 KOILDGVNVLHKKTAHFDLKPENIMLLDKNIPPHIKLIDFGLAHEIDEGVEFNINIGT 180
DB 121 KOILDGVNVLHKKTAHFDLKPENIMLLDKNIPPHIKLIDFGLAHEIDEGVEFNINIGT 180
QY 181 PEFAPEIYNVEPLGLEADMSIGVITYILLSGASPLGDTKQOETLANITSVSDPDEEF 240
DB 181 PEFAPEIYNVEPLGLEADMSIGVITYILLSGASPLGDTKQOETLANITSVSDPDEEF 240
QY 241 FSHTSSELAQDFIRKLVLKETRRKLTIOEALRHPWITPVNQOAMVRBSVNLNFRKQY 300
DB 241 FSHTSSELAQDFIRKLVLKETRRKLTIOEALRHPWITPVNQOAMVRBSVNLNFRKQY 300
QY 301 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDELNRCESDTEEDIAARRKALHPRRSSTS 360
DB 301 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDELNRCESDTEEDIAARRKALHPRRSSTS 360

RESULT 4
US-09-791-537-13590

Sequence 4, Application us/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13590
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-13590

Query Match 99.4%; Score 1835; DB 21; Length 370;
Best Local Similarity 99.7%; Pred. No. 3.5e-135;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPKQKQVEDFYDIGELSGGFATVKKCKREKSTGLEVAAKFIKKRQSRASRGVSREE 60
DB 1 MEPPKQKQVEDFYDIGELSGGFATVKKCKREKSTGLEVAAKFIKKRQSRASRGVSREE 70

Qy	61	IEREVSILRQVLAHHNVTTLADYENRPNDDVHILEVSGELPFLQAKSLSSEBATSST	120
Db	71	IEREVSILRQVLAHHNVTTLADYENRPNDDVHILEVSGELPFLQAKSLSSEBATSST	130
Qy	121	KQILDGVNYLHTKKAIAHFDLKPENIMLDDKNIPPHIKLIDFGLAHIEDGVCFKNI	180
Db	131	KQILDGVNYLHTKKAIAHFDLKPENIMLDDKNIPPHIKLIDFGLAHIEDGVCFKNI	190
Qy	181	PEPAPAEIVNTEPGLGEADMSIGVITYILLSGASPLDGTQOETLANITSVSYD	240
Db	191	PEPAPAEIVNTEPGLGEADMSIGVITYILLSGASPLDGTQOETLANITSVSYD	250
Qy	241	FSHSTSELAKDIEIKLTVAKETRRKLTIDEALRHMPITPVDDQOAMVRESVNL	300
Db	251	FSHSTSELAKDIEIKLTVAKETRRKLTIDEALRHMPITPVDDQOAMVRESVNL	310
Qy	301	VRRRWKLSFVSJLCNHLUTRSLSMKVYALRPDEDLRNCESDTEEDDIARRKALH	360
Db	311	VRRRWKLSFVSJLCNHLUTRSLSMKVYALRPDEDLRNCESDTEEDDIARRKALH	370

```

RESULT 5
US-09-791-537-108109
: Sequence 108109, Application US/09791537
:
: GENERAL INFORMATION:
: APPLICANT: Blonomix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 108109
:
: LENGTH: 370
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
: US-09-791-537-108109

```

Query Match	98.88;	Score 1824;	DB 21;	Length 370;
Best Local Similarity	99.28;	Pred. No. 2.5e-13;		
Matches 357; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	MEPRKOOKVDEPDYDIGELSGGOFATYKKRKESTGJGVAAKRTIKKROSAKRGVSREE	60
Dp	11	MEPRKOOKVEEDFYDIGELSGGOFATYKKRKESTGJGVAAKRTIKKROSAKRGVSREE	70
Qy	61	IIEREVSLILROYLHHNNYTTLLHDVYENRNTDVAHHIELVSGGELFPOFLAOKESLSEEAATSEFI	120
Dp	71	IIEREVSLILROYLHHNNYTTLLHDVYENRNTDVAHHIELVSGGELFPOFLAOKESLSEEAATSEFI	130
Qy	121	KOILDGVNNTLHTKKAIAFEDLAKPENIMLMDKNFIPIPHKLIDFCLAEHIEDGVGFKNIFGT	180
Dp	131	KOILDGVNNTLHTKKAIAFEDLAKPENIMLMDKNFIPIPHKLIDFCLAEHIEDGVGFKNIFGT	190
Qy	181	PEVVAPEIVNVEPAGLEADMSIGVITYILLSGASPFGLDTKQETLANITSVSYDDEEF	240
Dp	191	PEVVAPEIVNVEPAGLEADMSIGVITYILLSGASPFGLDTKQETLANITAVSYDDEEF	250
Qy	241	FSHSHSELAKOIFIKRLVYKETRKRLLTIOEALRHFWITPVMDQAMVRESVYNLENRRQY	300
Dp	251	FSQSHSELAKOIFIKRLVYKETRKRLLTIOEALRHFWITPVMDQAMVRESVYNLENRRQY	310
Qy	301	VRRRWKLSFISVLCNHLJTRS LMKKKVHLRDEDDLRNCESTDEEDIAARRKALHRRRSSTS	360
Dp	311	VRRRWKLSFISVLCNHLJTRS LMKKKVHLRDEDDLRNCESTDEEDIAARRKALHRRRSSTS	370

RESULT 6
US-09-791-537-108110

```

: Sequence 108110. Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Blomomix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 108110
: LENGTH: 370
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-791-537-108110

Query Match          95.6%   Score 1764   DB-21:   Length 370;
Best Local Similarity 96.4%   Pred. No. 1,3e+19;
Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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Qy	1	MEPFQOQVVEDPYDIDGEEELGSGQFPAIVKCKRKSNGLETAAPFIKKRGRASRGRVSRBE	60
Dp	11	MEPFQOQVVEDPYDIDGEEELGSGQFPAIVKCKRKSNGLETAAPFIKKRGRASRGRVSRBE	70
Qy	61	IEREVSILROYAHNVITLHDVYENRPTDVHILELVSGGELFDPLAQKESLSEEEATSTI	120
Dp	71	IEREVSILROYAHNVITLHDVYENRPTDVHILELVSGGELFDPLAQKESLSEEEATSTI	130
Qy	121	KOILDGAVNYLHTKKLAHFELKPEKNIMLDDKNPIPIHKLIDFGLAHEIDGVEFNIFET	180
Dp	131	KOILDGAVNYLHTKKLAHFELKPEKNIMLDDKNPIPIHKLIDFGLAHEIDGVEFNIFET	190
Qy	181	PEFVAPEIYNEPTLDEADMSIGVITYITLLSGASPFLODTQOETLANITSYSDPDEEF	240
Dp	191	PEFVAPEIYNEPTLDEADMSIGVITYITLLSGASPFLODTQOETLANITSYSDPDEEF	250
Qy	241	FSHTSELAKDFIRKLLVKEETRKRRLTIOEALRHPWITPVDOQAMVRESVNLLENFRKQY	300
Dp	251	FSHTSELAKDFIRKLLVKEETRKRRLTIOEALRHPWITPVDOQAMVRESVNLLENFRKQY	310
Qy	301	VRRRRKLSFSIYSLCNHLTRLSLMKVVHLRPDDDLKNCESDTEBDIARRKALHPRRRSSIS	360
Dp	311	VRRRRKLSFSIYSLCNHLTRLSLMKVVHLRTSDLNCESDTEBDIENIARRKALHPRRRSSIS	370

```

RESULT 7
PCT-US01-08631-39633
: Sequence 39633, Application PC/TUS0108631
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc
: TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
: FILE REFERENCE: 21272-049
: CURRENT APPLICATION NUMBER: PCT/US01/08631
: CURRENT FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: 09/540,217
: PRIOR FILING DATE: 2000-03-31
: PRIOR APPLICATION NUMBER: 09/649,167
: PRIOR FILING DATE: 2000-08-23
: NUMBER OF SEQ ID NOS: 60736
: SOFTWARE: Custom
: SEQ ID NO 39633
: LENGTH: 359
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (128)..(147)
: OTHER INFORMATION: TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE domain identified
: OTHER INFORMATION: by eMUTRIX, accession number PR00109B, p-value=7.055e-11, raw
: NAME/KEY: DOMAIN

```



```
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49880
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-49880
```

```
Query Match
Best Local Similarity 68.2%; Pred. No. 6.9e-92;
Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2;
```

```
OY 1 MEFPEKQKVEDFYDIGEELSGOFAIVKKCREKSTGLEAAKFIKKRQSRASHRGVSREE 60
   1 MTFVRENDVDYDTGEELSGOFAVKKCREKSTGLQYAAKFIKKRRTKSSRGRVSRED 60
DB
OY 61 IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
   IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
DB 61 IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
OY 121 KQILDGVNLTHTKIAHFDLKPENIMLDKNIPPHIKLIDFGLAHEIDEGVEFKNI 180
   121 KQILNGVYLLHSQIAHFDLKPENIMLDKNVPKPKIKIIDFGLAHEIDEGVEFKNI 180
DB 121 KQILNGVYLLHSQIAHFDLKPENIMLDKNVPKPKIKIIDFGLAHEIDEGVEFKNI 180
OY 181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
   181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
DB 181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
OY 241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
   241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
DB 241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
OY 301 VRRRWKLSFISVSLCNHLTRSLMKKVHL--RPDEDLRNCSDETEEDDIARRKALH 352
   301 ARKKWKQSVRLSLCQRLSRFSLSRSMVSARSDDTL-----DEEDSFVKALITH 350
DB 301 ARKKWKQSVRLSLCQRLSRFSLSRSMVSARSDDTL-----DEEDSFVKALITH 350
```

```
RESULT 11
US-60-350-061-273
; Sequence 273, Application US/60350061
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; FILE REFERENCE: D0185
; CURRENT APPLICATION NUMBER: US/60/350,061
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-350-061-273
```

```
Query Match
Best Local Similarity 70.0%; Score 1293; DB 27; Length 1431;
Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2;
```

```
OY 1 MEFPEKQKVEDFYDIGEELSGOFAIVKKCREKSTGLEAAKFIKKRQSRASHRGVSREE 60
   1 MTFVRENDVDYDTGEELSGOFAVKKCREKSTGLQYAAKFIKKRRTKSSRGRVSRED 60
DB
OY 61 IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
   IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
DB 61 IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
OY 121 KQILDGVNLTHTKIAHFDLKPENIMLDKNIPPHIKLIDFGLAHEIDEGVEFKNI 180
   121 KQILNGVYLLHSQIAHFDLKPENIMLDKNVPKPKIKIIDFGLAHEIDEGVEFKNI 180
DB 121 KQILNGVYLLHSQIAHFDLKPENIMLDKNVPKPKIKIIDFGLAHEIDEGVEFKNI 180
```

```
DB 121 KQILNGVYLLHSQIAHFDLKPENIMLDKNVPKPKIKIIDFGLAHEIDEGVEFKNI 180
OY 181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
   181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
DB 181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
OY 241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
   241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
DB 241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
OY 301 VRRRWKLSFISVSLCNHLTRSLMKKVHL--RPDEDLRNCSDETEEDDIARRKALH 352
   301 ARKKWKQSVRLSLCQRLSRFSLSRSMVSARSDDTL-----DEEDSFVKALITH 350
DB 301 ARKKWKQSVRLSLCQRLSRFSLSRSMVSARSDDTL-----DEEDSFVKALITH 350
```

```
RESULT 12
US-60-375-626-6
; Sequence 6, Application US/60375626
; GENERAL INFORMATION:
; APPLICANT: Welch, Nadine
; TITLE OF INVENTION: Methods and compositions for treating
; FILE REFERENCE: MP102-063PI(M)
; CURRENT APPLICATION NUMBER: US/60/375,626
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Homosapien
US-60-375-626-6
```

```
Query Match
Best Local Similarity 70.0%; Score 1293; DB 27; Length 1431;
Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2;
```

```
OY 1 MEFPEKQKVEDFYDIGEELSGOFAIVKKCREKSTGLEAAKFIKKRQSRASHRGVSREE 60
   1 MTFVRENDVDYDTGEELSGOFAVKKCREKSTGLQYAAKFIKKRRTKSSRGRVSRED 60
DB
OY 61 IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
   IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
DB 61 IEREVSILKQVLHNHYITLHDYENRTDVNHLIELVSGGELDFPLAOKESLSEETATSF 120
OY 121 KQILDGVNLTHTKIAHFDLKPENIMLDKNIPPHIKLIDFGLAHEIDEGVEFKNI 180
   121 KQILNGVYLLHSQIAHFDLKPENIMLDKNVPKPKIKIIDFGLAHEIDEGVEFKNI 180
DB 121 KQILNGVYLLHSQIAHFDLKPENIMLDKNVPKPKIKIIDFGLAHEIDEGVEFKNI 180
OY 181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
   181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
DB 181 PEVVAPEIYNEPRLGLEADWMSIGVITYLLSGASPLDGTQOETLANITSVSYDDEEF 240
OY 241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
   241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
DB 241 FSHSTELANDFIRKLKLVKTRKRLTIOEALRHWMITPVNOQAMVRESVNLNENRKQY 300
OY 301 VRRRWKLSFISVSLCNHLTRSLMKKVHL--RPDEDLRNCSDETEEDDIARRKALH 352
   301 ARKKWKQSVRLSLCQRLSRFSLSRSMVSARSDDTL-----DEEDSFVKALITH 350
DB 301 ARKKWKQSVRLSLCQRLSRFSLSRSMVSARSDDTL-----DEEDSFVKALITH 350
```

```
RESULT 13
US-08-810-712-10
; Sequence 10, Application US/08810712F
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co. LTD
; TITLE OF INVENTION: Tumor Suppressor Genes, Proteins Encoded Thereby and
; FILE REFERENCE: Yeda-Adi Kimchi
; CURRENT APPLICATION NUMBER: US/08/810,712F
; CURRENT FILING DATE: 1997-03-03
; EARLIER APPLICATION NUMBER: PCT/US94/11598
```

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: EARLIER FILING DATE: 1994-10-12
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10
: LENGTH: 1423
: TYPE: prt
: ORGANISM: Homo sapiens
US-08-810-712-10

```

Query Match	67.6%	Score 1248;	DB 12	Length 1423;
Best Local Similarity	66.5%	Pred. No. 2.3e-88;		
Matches 236;	Conservative 60;	Mismatches 43;	Indels 16;	Gaps 3.

OY	1	MEPRKOQVDEFPYDIGEELSGGQPAIKKOREMSITGLYEAKLTKRKUSASVKGSKE	60
	1	: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	1	MTVFROENVDDYUPTGELSGGCFAYAVKKCREKSTGYQYPAKFKTRKRSTSRRGYSRED	60
OY	61	TEREVSTILROYLNHNVITLIHDVYENRNDVVYLIELLEVSGBGLPFOIAOKESLTSEEDTSFI	120
	61	: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	61	TEREVSTILKEQHNPVPIVTLHVYENKNKDVIILIEVLVAGELFDPLAKESULTTEEBATEPL	120
	61	: : : : : : : : : : : : : : : : : : : : : : : : :	
OY	121	KOILDGVUYLTHTTKIAPHDLKPENIMELDKNIPRIPIKLIDFGLAHEIEDGEVEKNIFGT	180
	121	: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	121	KOILNGVYYLSLOLAHDELKPENIMELDRNVAPRIKIIDF-----GNESKNIFGT	172
OY	161	PEPVAPETVANYEPGLEMDMSIGVTITYILISGASPFLGDTKOETTANITSVADPEDEF	240
	161	: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	173	PEVPAPETVANYEPGLEMDMSGVITYITYILISGASPFLGDTKOETLANVASVNEPEDEX	232
OY	241	FHSHTSELAKDFIRLLIKLYETRKRRLTIOEARLPWITVDNOQAMRVRESVYNLENREKY	300
	241	: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	233	FHSNTSALMKDPIRLRLLVDPKKRMTOISLOHPWIKRPDOALSRAKSAVNMEKFKA	292
OY	301	VARRBKLSFSYSLCJCNHLTFRSLMKVUH---RPDEDLRNCSDPEEDIARAKHAL	352
	301	: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	293	AKKKMKOSVRLSTLCQRLSRSPFLSRSMNSVARSDTL-----DEDSFWYKAIH	342

```

RESULT 14
US-09-380-159-12
; Sequence 12, Application US/09380159
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Company Ltd.
; TITLE OF INVENTION: Compositions for Treatment of Disorders Involving
; TITLE OF INVENTION: Programmed Cell Death
; FILE REFERENCE: YEDA (KIMCHI)
; CURRENT APPLICATION NUMBER: US/09/380,159
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: PCT/IL 98/00102
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1423
; TYPE: prt
; ORGANISM: HUMAN
US-09-380-159-12

```

Query Match	Similarity	67.6%	Score 1248:	DB 17:	Length 1423:
Best Local	Similarity	66.5%	Pred. No. 2.3e-88		
Matches	Conservative	60:	Mismatches	43:	Indels 16: Gaps 3:
Qy	1	MEPFKQGVADFPDICEIGELSGGOFATVKKCKREKSTGLEAFAKIKRKQSRASRRGVSRRE	60		
Db	1	MYFPRQINADVDDYDTGELSGGOFAYVKKCKREKSTGLQYPAKTIKKRKRRKSSRGVSRRE	60		
Qy	61	IEREVSILLRQVLLHHNVITLHDVYENRTDVVHILELVSGGELFDFLLAQKBSLSEETSF	120		
Db	61	IEREVSILKEIQHPNVITLHEVYENKTDVILLIELVAGGELFDFLLAKEBSLSEETSF	120		
Qy	121	KQILDGNYNLHTKKIAHFDLAKPENIMIMLDKNIPILPHIKLIDFCLAHIEDGVFEKNINFG	180		
Db	121	KQINGNYVYLQIAIHFDLAKPENIMIMLDNVPKPKIIDF-----GNEFKINFG	172		

QY	181	PEPAPELVEVNERPEGLERADMMISGIVITUYILLISGASPELGOTKOETLANIRSVASDPEEE	240
	173	PEPAPELVEVNERPEGLERADMMISGIVITUYILLISGASPELGOTKOETLANISAVNTEPEDEY	232
QY	241	FHSHTSELAKDIFIRKLVEKPPKRLTIOEALRHPMIVPDNOQAAVRESVAVNLENFRKQY	300
	233	FSNSTRALAKDIFIRKLVEKPPKRLTIOEALRHPMIVPDNOQAAVRESVAVNLENFRKQY	292
QY	301	VRRRRKLSFVSIVSCNHLTRSLMKVHL---RPDEDLRNCESDTEEDJARRKALH	352
	293	ARKKKHGVRLISLCQRSLRSFLEBSRMNMSVARSDTL-----DEDSFVYKAIH	342

```

RESULT 15
US-09-791-537-6033
; Sequence 6033, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: patentIn version 3.0
; SEQ ID NO 6033
; LENGTH: 1423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-6033

```

Query Match	Similarity	67.6%	Score 1248	DB 21	Length 1423
Best Local	Similarity	66.5%	Pred. No. 2.3e-81		
Matches	236	Conservative	60	Mismatches 43	Indels 16
					Gaps 3
Qy	1	MEPFKQAKVEDFDGEEELGSGCFALVKKCKREKSTGLEVAAAFIKRKQSRASHRGVSRBE	60		
		: : : : : : : : : : : : : : : : : : : : : : : :			
Db	1	MYVFRQENVDYDYGEEELGSGCFANVKKCKREKSTGLQPAKTIKRRKSSRGVSRBE	60		
Qy	61	IEREVSILRQVLHHNVITLHDVYENFTDVVHILEVSGGELDFDLQKESLSSEETST	120		
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	61	IEREVSILKEIHPNVITLHEVYENKTDVILILEVAGSELDFDLQKESLSSEETATEL	120		
Qy	121	KQLDSVNLHTKTKIAHFDLPKPNIMLLDKNPIPIHKILIDFLAHIEDGVFEKKIIFET	180		
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	121	KQLNCGVYLLQLQIAHFDLPKPNIMLLDKNVPKRIKIIDF-----GNEFKKIIFET	172		
Qy	181	PEFVAPEIYVPEPLGLEADMMSIGVITVYLLSGASPELDGTQKQETLANITSVSYDDEEF	240		
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	173	PEFVAPEIYVPEPLGLEADMMSIGVITVYLLSGASPELDGTQKQETLANVAVNYEEDEY	232		
Qy	241	FSHTSELAKDFIRKLKVKETRRKRLTQDALRHPIITPVNQOAMVRESVYNLENRRKQY	300		
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	233	FSMTSLAKDFIRRLLYLVKDPKKRMTTQDSLOAHWIKRFDQOALSRSKASVNNKEKRFKA	292		
Qy	301	VRRRRKLSTFSLVLCNHLTSLKKKYHL---RPDEDLRNCSTPEEDIAARKLH	352		
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	293	ARRKKQSVRLISLQORLSRFLSRKMSVARSDDTL-----DEEDSFVKALIH	342		

Search completed: March 26, 2003, 19:16:06
Job time : 163.064 secs

11

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:09:46 ; Search time 28.3146 Seconds
(without alignments)
1678.167 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846
Sequence: 1 MEPPKQKQVEDFYDIGELG.....TIEDIARRKALHPRRSSTS 360

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 613006 seqs, 131990659 residues

Total number of hits satisfying chosen parameters: 613006

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents-AA-New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US05_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1824	98.8	370	7	US-60-443-566-3011 Sequence 3011, Ap
2	1293	70.0	1431	1	PCT-US03-02484-38 Sequence 38, Appl
3	1293	70.0	1431	5	US-09-949-002-377 Sequence 377, App
4	1293	70.0	1431	6	US-10-348-119-220 Sequence 220, App
5	1293	70.0	1436	7	US-60-443-566-4055 Sequence 4055, Ap
6	1224	66.3	1412	5	US-09-949-002-486 Sequence 486, App
7	1166	63.2	454	1	PCT-US02-31357-119 Sequence 119, App
8	1166	63.2	454	6	US-10-262-445-119 Sequence 119, App
9	1166	63.2	454	7	US-60-443-566-2831 Sequence 2831, Ap
10	1161	62.9	282	5	US-09-724-676-69504 Sequence 69504, A
11	1161	62.9	282	5	US-09-724-676-69504 Sequence 69504, A
12	1153	62.5	595	5	US-09-724-676-69506 Sequence 69506, A
13	1153	62.5	595	5	US-09-724-676-69506 Sequence 69506, A
14	677.5	36.7	298	6	US-10-274-978-18 Sequence 18, Appl
15	668.5	36.2	414	6	US-60-443-566-2540 Sequence 2540, Ap
16	665.5	36.1	2783	6	US-10-369-493-6344 Sequence 6344, Ap
17	664.5	36.0	508	6	US-10-274-978-19 Sequence 19, Appl
18	641.5	34.8	372	7	US-60-443-566-2980 Sequence 2980, Ap
19	574.5	31.1	596	6	US-10-311-034-6 Sequence 6, Appl1
20	564	30.6	355	6	US-10-258-106-11 Sequence 11, Appl1
21	564	30.6	357	6	US-10-258-106-2 Sequence 2, Appl1
22	564	30.6	357	7	US-60-435-108-2 Sequence 2, Appl1
23	536	30.1	355	6	US-10-355-975-10 Sequence 10, Appl1
24	543.5	29.4	460	7	US-60-443-566-3356 Sequence 3356, Ap
25	543.5	29.4	476	7	US-60-443-566-3355 Sequence 3355, Ap
26	530.5	28.7	370	6	US-10-300-828-4 Sequence 4, Appl1

27	530.5	28.7	846	6	US-10-274-978-4	Sequence 4, Appl1
28	530.5	28.7	2380	6	US-10-333-314-18	Sequence 18, Appl1
29	530.5	28.7	3267	1	PCT-US02-33723-28	Sequence 28, Appl1
30	530	28.7	473	1	PCT-US02-40194-15	Sequence 15, Appl1
31	530	28.7	473	6	US-10-320-351-15	Sequence 15, Appl1
32	528.5	28.6	499	6	PCT-US03-02588-88	Sequence 88, Appl1
33	528.5	28.6	499	6	US-10-354-358-88	Sequence 88, Appl1
34	526	28.5	549	6	US-10-274-978-6	Sequence 6, Appl1
35	519.5	28.1	533	6	US-10-160-619-176	Sequence 176, Appl1
36	518	28.1	515	6	US-10-160-619-66	Sequence 66, Appl1
37	512	27.7	414	6	US-10-274-978-14	Sequence 14, Appl1
38	512	27.7	2861	1	PCT-US02-14877A-687	Sequence 687, App
39	512	27.7	2861	6	US-10-240-851-108	Sequence 108, App
40	512	27.7	2861	6	US-10-099-056-1370	Sequence 1370, Ap
41	512	27.7	3038	6	US-10-274-462-26	Sequence 26, Appl1
42	507.5	27.5	556	1	PCT-US02-33723-19	Sequence 19, Appl1
43	503.5	27.3	588	6	US-10-311-034-22	Sequence 22, Appl1
44	500.5	27.1	338	6	US-10-264-237-2792	Sequence 2792, Ap
45	500	27.1	274	6	US-10-274-978-15	Sequence 15, Appl1

ALIGNMENTS

RESULT 1
US-60-443-566-3011
; Sequence 3011, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001447
; CURRENT APPLICATION NUMBER: US/60/443,566
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 25102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3011
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-443-566-3011

Query Match 98.8%; Score 1824; DB 7; Length 370;
Best Local Similarity 99.2%; Pred. No. 3e-157;
Matches 357; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MEPPKQKQVEDFYDIGELSGGFAIYKCKREKSTGLEAYAKFIKKRSRSGVRSRE	60
DB	11	MEPPKQKQVEDFYDIGELSGGFAIYKCKREKSTGLEAYAKFIKKRSRSGVRSRE	70
QY	61	IEREVSILROYLHHNVITLHDVYENRTDVYHIELVSGGELFDELAOKESLSEBEATSFI	120
DB	71	IEREVSILROYLHHNVITLHDVYENRTDVYHIELVSGGELFDELAOKESLSEBEATSFI	130
QY	121	KQILDGNYVLTAKIAFDLKPENIMLDKNIPRPHKILDFGLAHIEGVEKKNFTGT	180
DB	131	KQILDGNYVLTAKIAFDLKPENIMLDKNIPRPHKILDFGLAHIEGVEKKNFTGT	190
QY	181	PEFYAPFVWVEPEGLGADWMSIGVITYLLSGASPLGDTKQETLANITAVSDPDEEF	240
DB	191	PEFYAPFVWVEPEGLGADWMSIGVITYLLSGASPLGDTKQETLANITAVSDPDEEF	250
QY	241	FSHTSELAKDFIRKLAVKETRRKRLTIOEALRHPWITVDNQOAVRRESVYNLENFRKQY	300
DB	251	FSHTSELAKDFIRKLAVKETRRKRLTIOEALRHPWITVDNQOAVRRESVYNLENFRKQY	310
QY	301	VRRRWKLSFYSIVSLCNHLTSLMKVHLRDEDELKNCESDTEEDIARRKALHPRRSSTS	360
DB	311	VRRRWKLSFYSIVSLCNHLTSLMKVHLRDEDELKNCESDTEEDIARRKALHPRRSSTS	370

RESULT 2

[illegible]

```

RESULT 3
US-09-949-002-377
: Sequence 377, Application US/09949002
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CLO00790
: CURRENT APPLICATION NUMBER: US/09/949,002
: CURRENT FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: 60/231,401
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 10823
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 377
: LENGTH: 1431
: TYPE: PRT
: ORGANISM: Human
US-09-949-002-377

```

```

Query March          70.0%: Score 1293; DB 5; Length 1431;
Best Local Similarity    68.2%; Pred. No. 3e-108;
Matches   242; Conservative      62; Mismatches   43; Indels     8; Gaps       2;

Qy      1 MEFFROAKVEPEFYDIGSELGSGFAIVYKRCREKSTGTLEYAKFTIKRKQRASRGRVAREE 60
         | :| :|||:||| |||||||:|||||:|||||:|||||:|||||:
Db      1 MYVFQGNVDNDYYDIGELGSGGFAYVKKCKEKSTGLGYAKFKTKRYTKSSRRGVAREED 60
Qy      61 IEREVSILROYLHHNVTLHDVYEKNRTDYVIHILEYSGGELFDFPLACKESI.SEEEAISFI 120
         |||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~|:|:|:|:
Db      61 IEREVISLKIEIHPNVTITLHEVYEKNRTDVIIILELVAGGELEDP LAEEKSELTSEEAEFL 120
Qy      121 KQILDGVNLTHHKTAHFHFDKPENIMLDKNPIPHIKLIDFGLAHEIEDVEEFKNIFGT 180
        |||||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      121 KQLNGVYLTHLSLOAHEDKLKENIMLDRNPVKRIIIDPGLAHKIDPFNEEKNIFGT 180
Qy      181 PEFPVAPEIYNVEPPLGLEADMMSIGVITYILLGSASPFLGDTRKOETLANITSYSTDPDEEF 240
        |||||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~|:|:|:|:
Db      181 PEFVAPEIYNVEPPLGLEADMMSGIVITYILLGSASPFLGDTRKOETLANIVSAVNEYFEDEX 240
Qy      241 FSHTSLADLFIRKLLVETKRRLTIOEARLPMTTPPDNOOAMVRRESVNLENFRKQY 300
        |||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~|:|:|:|:
Db      241 FSNTSLADEFTRLVLVDPKKRTIODSLOHPWIKPKOTQOALSRRKSAAVMKEKFKA 300
Qy      301 VRRKKLFSIYSICNHLTRSIAMKKVVHL---RPDEDLRNCSDYTEEDIARRALH 352
        |||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~|:|:|:|:
Db      301 ARKKMKQSRLISLCORLSRFSLSRSMNSVANSDDTL-----DEEDSVMAAIIH 350

RESULT 4
US-10-348-119-220
; Sequence 220, Application US/10348119
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 NP
; CURRENT APPLICATION NUMBER: US/10/348,119
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 220
; LENGTH: 1431
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-348-119-220

Query Match          70.0%; Score 1293; DB 6; Length 1431;
```


Best Local Similarity 68.2%; Pred. No. 3e-108;
Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2

[illegible]

RESULT 5
US-60-443-566-4055

```

: Sequence 4055, Application US/60443566
:
: GENERAL INFORMATION:
:
: APPLICANT: CARGILL, Michele
:
: APPLICANT: BEGOVICH, Ann
:
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
:
: TITLE OF INVENTION: RHUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
:
: FILE REFERENCE: CL001447
:
: CURRENT APPLICATION NUMBER: US/60/443,566
:
: CURRENT FILING DATE: 2003-01-30
:
: NUMBER OF SEQ. ID NOS: 25102
:
: SOFTWARE: FASTSEQ for Windows Version 4.0
:
: SEQ ID NO 4055
:
: LENGTH: 1436
:
: TYPE: PR1
:
: ORGANISM: Homo sapiens
:
: US-60-443-566-4055

```

Query Match	70.0%	Score 1293	DB 7	Length 1436
Best Local Similarity	68.2%	Pred. 10.3e-108		
Matches 242: Conservative	62:	Mismatches 43:	Indels 8:	Gaps 2

Qy	1	MEPFOQKVEDFPVDIGELLSGQFAIVKCKREKSTGLEVAFKIKKRQSHASRGVSREB	60
Db	1	MTFEROENVDVYDTGSELSSGQFAVVKCKREKSTGLQYAKFKIKKRRTSSRRGVSRED	60
Qy	61	IEREVSLTROVLLHNVTTLHDYENRDRVYHLEIVSGGELFPLQKESLSREAYTSFI	120
Db	61	IEREVSLTKETQHPNVTTLHEVYENKRDVLLLELVAGGELFPLQKESLTHEEATEFI	120
Qy	121	KQILDGVNYLHTKTHIAHDEKRPENIMLLDKNIEPIPHIKLDFCLAEHIEDGVCFKNI	180
Db	121	KQILNGVYUHLSDQIAHFDLKPENIMLLDRNVPKPRIKIDFGLAKHIDFGNEFKNI	180
Qy	181	PEFAPAEIVNEPGLGELADMMSTGVITYLLLSGASPLSGTKOETLANITSVSYDDEE	240
Db	181	PEFAPAEIVNEPGLGELADMMISGVITYLLLSGASPLSGTKOETLANIVSAVVEEDEE	240
Qy	241	FSHSELAQDFIRKLIVKETRKRLLTIOEALRHWITPVDVQOAMVRESVNLNENRKOY	300
Db	241	FSNLSLAKDQFIRRLKLDPKRKRRITIDDSLOHHPWIKRKPDQOALSRAKSAVNNKKRKA	300
Qy	301	VRRRWKLSFSLVSCJNHLTSLMKKVHL---RPDEDLRNCSDEPTIEDIARAKALH	352

Db 301 ARKKWKQSVRLISLCQRLSRFSLSRSNMSVARSDTL-----DEEDSFVMAIIH 3500

```

RESULT 6
US-09-949-002-486
: Sequence 486, Application US/09949002
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CL000790
: CURRENT APPLICATION NUMBER: US/09/949,002
: CURRENT FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: 60/231,401
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 10823
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 486
: LENGTH: 1412
: TYPE: PRF
: ORGANISM: Human
: US-09-949-002-486

```

Query Match	66.3%	Score 1224	DB 5	Length 1412
Best Local Similarity	68.5%	Pred. No. 5.4e-102		
Matches 231	Conservative 58	Mismatches 40	Indels 8	Gaps 2

QY	19	LGSGFAIVKKCKREKSTGLEAAFIKKRQSRASRGVSRREIEEVSILQOVLHNNVIT	78
		1	LFSGFAVAVKKCKREKSTGLOAAAFIKKRKRKSSRGVSRREIEEVSILKEIOHPNVIT
Db			60
QY	79	LHDVYENKTDVVIILEVSGGELFDPLAOKTSLSEEAFTSPKOILQOVNVLHTPKIAHF	138
Db	61	LHEVYENKTDVLIILEVAGGELFDFLEAKESLVEEETEPFKOQLNVLVYLLHSIQIAHF	120
QY	139	DLKPEINMLDKNIPPIPIKILIDFGLAHEIEDGVENKIFGTPPEFAVEIYNEPGLGEA	198
Db	121	DLKPEINMLDNRNPKPIKRIIDFGLAHKIDFGNENFKIIFGTPPEFAVEIYNEPGLGEA	180
QY	199	DMMSIGVITYIYLLSGASPLDGTQOETLANITSVSYDEDEEFSTSLANDFIRKLLVY	258
Db	181	DMMSIGVITYIYLLSGASPLDGTQOETLANISAVNYEFDEEYFSTSLANDFIRKLLVY	240
QY	259	ETKRRLTIQELRHPWITPVUNQOAMVRRSEVNVLENFKQYVRRRKLSTSYSLCNHL	318
Db	241	DPKKRMTIODSLQHPWIKPDKTQOALSKKASAVNMKEFKFAARAKKWKQSYVLLISICORL	300
QY	319	TRSLMKKXVHL---RPDEDLRNCESDTEEDIDARRKALH	352
Db	301	SRSFSLSRMSNMSVARSDDTL---DEEDSFVAKALIH	332

```

RESULT 7
PCT-US02-31357-119
: Sequence 119, Application PC/TUS0231357
: GENERAL INFORMATION:
: APPLICANT: CutaGen Corporation, et al
: TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
: TITLE OF INVENTION: THE SAME
: FILE REFERENCE: 21402-462D-061
: CURRENT APPLICATION NUMBER: PCT/US02/31357
: CURRENT FILING DATE: 2002-10-02
: PRIOR APPLICATION NUMBER: 60/327,454
: PRIOR FILING DATE: 2001-10-05
: PRIOR APPLICATION NUMBER: 60/327,917
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/328,029
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/328,056
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/328,849
: PRIOR FILING DATE: 2001-10-12

```

```

; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 119
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-31357-119

```

```

Query Match      63.2%; Score 1166; DB 1; Length 454;
Best Local Similarity 64.7%; Pred. No. 1.9e-97;
Matches 233; Conservative 49; Mismatches 60; Indels 18; Gaps 3;

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QY 1 MEFKQKVEDFYDIGEELSGQFAIVKCKRKSTGLEAAKFIKKROSRRGVSREE 60
D 1 MEFKQKVEDFYDIGEELSGQFAIVKCKRKSTGLEAAKFIKKROSRRGVSREE 60
QY 61 IREVSILROVYHNHNVITLHDYENRTDVVHLLVSGELDFDLAKESLSEEBATSF 120
D 61 IREVSILROVYHNHNVITLHDYENRTDVVHLLVSGELDFDLAKESLSEEBATSF 120
QY 121 KOILGVNLTAKKTAHFDLKPENIMLDKNIPPIKILIDFGLAHEIDGVEFNKIFGT 180
D 121 KOILGVNLTAKKTAHFDLKPENIMLDKNIPPIKILIDFGLAHEIDGVEFNKIFGT 180
QY 181 PEFVAPETVNYEPPLGLEADMSIGVITYLLSGASPLGDTQOETLANITSYDPDEF 240
D 181 PEFVAPETVNYEPPLGLEADMSIGVITYLLSGASPLGDTQOETLANITSYDPDEF 240
QY 241 FSHTSFLAKDFIRKLIVKTRKRLTIOELRHPWITPVNOQAMVRESVNLNFRKQY 300
D 241 FSHTSFLAKDFIRKLIVKTRKRLTIOELRHPWITPVNOQAMVRESVNLNFRKQY 300
QY 301 VRRRWKLSFVSLCNHLTRSLMKKYNLRPDE---DLRNCSDTEEDIAKKALHRRRS 357
D 301 VRRRWKLSFVSLCNHLTRSLMKKYNLRPDE---DLRNCSDTEEDIAKKALHRRRS 357
D 294 RRLKTRTLREKTYIKSHS-----LPPNNSYADFERFSKYLEBAAAAEGLRELQRS 345

```

```

RESULT 8
US-10-262-445-119
; Sequence 119, Application US/10262445
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Caterton, Elina
; APPLICANT: Chan, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Glot, Lotc
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kikuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei

```

```

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHOD
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 119
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-445-119

```

```

Query Match      63.2%; Score 1166; DB 6; Length 454;
Best Local Similarity 64.7%; Pred. No. 1.9e-97;
Matches 233; Conservative 49; Mismatches 60; Indels 18; Gaps 3;

```

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QY 1 MEFKQKVEDFYDIGEELSGQFAIVKCKRKSTGLEAAKFIKKROSRRGVSREE 60
D 1 MEFKQKVEDFYDIGEELSGQFAIVKCKRKSTGLEAAKFIKKROSRRGVSREE 60
QY 61 IREVSILROVYHNHNVITLHDYENRTDVVHLLVSGELDFDLAKESLSEEBATSF 120
D 61 IREVSILROVYHNHNVITLHDYENRTDVVHLLVSGELDFDLAKESLSEEBATSF 120
QY 121 KOILGVNLTAKKTAHFDLKPENIMLDKNIPPIKILIDFGLAHEIDGVEFNKIFGT 180
D 121 KOILGVNLTAKKTAHFDLKPENIMLDKNIPPIKILIDFGLAHEIDGVEFNKIFGT 180
QY 181 PEFVAPETVNYEPPLGLEADMSIGVITYLLSGASPLGDTQOETLANITSYDPDEF 240
D 181 PEFVAPETVNYEPPLGLEADMSIGVITYLLSGASPLGDTQOETLANITSYDPDEF 240
QY 241 FSHTSFLAKDFIRKLIVKTRKRLTIOELRHPWITPVNOQAMVRESVNLNFRKQY 300
D 241 FSHTSFLAKDFIRKLIVKTRKRLTIOELRHPWITPVNOQAMVRESVNLNFRKQY 300
QY 301 VRRRWKLSFVSLCNHLTRSLMKKYNLRPDE---DLRNCSDTEEDIAKKALHRRRS 357
D 301 VRRRWKLSFVSLCNHLTRSLMKKYNLRPDE---DLRNCSDTEEDIAKKALHRRRS 357
D 294 RRLKTRTLREKTYIKSHS-----LPPNNSYADFERFSKYLEBAAAAEGLRELQRS 345

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RESULT 9
US-60-443-566-2831
; Sequence 2831, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001447
; CURRENT APPLICATION NUMBER: US/60/443,566

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;; CURRENT FILING DATE: 2003-01-30
;; NUMBER OF SEQ ID NOS: 25102
;; SOFTWARE: PastSeq for Windows Version 4.0
;; SEQ ID NO 2831
;; LENGTH: 454
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-60-443-566-2831

Query Match 63.2%; Score 1166; DB 7; Length 454;
Best Local Similarity 64.7%; Pred. No. 1.9e-97;
Matches 233; Conservative 49; Mismatches 60; Indels 18; Gaps 3;

OY 1 MEFPOKQKVEDFYDGEELGSGOFATVKKCREKSTGLEVAAFKIKKROASRGVSREE 60
DB 1 MSTFQEDVEDHDEYEMGEELGSGOFALVRKCRQGTGEYAAKFKIKRRSSSRGVSRRE 60
OY 61 IREVSILROVLHNVITLHDYENRTDVVHILEVSGELDFPLAOKESLSEEXTSFT 120
DB 61 IREVNILREIRHPNITLHDIFENKTDVLLLELVSGELDFLAEKESLSEEXTSFT 120
OY 121 KOILDGVNLTHTKKAHFDLKPENIMLDKNIPRIKIDFGLAHEIDEGVEFKNIFGT 180
DB 121 KOILDGVNLTHTKKAHFDLKPENIMLDKNVNPRIKIDFGIAHKIEAGNEFKNIFGT 180
OY 181 PEFVAPEIVNYEPLGLEADWMSIGVTYILLSGASPLGDTKQETLANTSYSDDEEF 240
DB 181 PEFVAPEIVNYEPLGLEADWMSIGVTYILLSGASPLGDTKQETLNTSAVYDDEEF 240
OY 241 FSHTSSELAKDFIRKLKLVKTRKRLTQDALRHPWITPVNOQAMVRESVNLLENFRKOY 300
DB 241 FSNITSELAKDFIRRLLVKDPKRRMTIAOSLEHSMWT-----KAIRRRNVREGDSGRKE 293
OY 301 VRRRKLSFVSICNLHTLSIMKKVHLRDE--DLRNCESDTEEDIRAKALHPRRRS 357
DB 294 RRRLKTRTKRYTIKSHS-----LPPNNSYADFERFSKVLFEAAMAEGLRELQRS 345

RESULT 10

US-09-724-676-69504
;; Sequence 69504, Application US/09724676
;; GENERAL INFORMATION:
;; APPLICANT: Compugen LTD
;; TITLE OF INVENTION: Variants of alternative splicing
;; FILE REFERENCE: 129181.4 Compugen
;; CURRENT APPLICATION NUMBER: US/09/724,676
;; CURRENT FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 97222
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 69504
;; LENGTH: 282
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (276)..(276)
;; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-724-676-69504

Query Match 62.9%; Score 1161; DB 5; Length 282;
Best Local Similarity 78.1%; Pred. No. 2.7e-97;
Matches 217; Conservative 39; Mismatches 22; Indels 0; Gaps 0;

OY 1 MEFPOKQKVEDFYDGEELGSGOFATVKKCREKSTGLEVAAFKIKKROASRGVSREE 60
DB 1 MSTFQEDVEDHDEYEMGEELGSGOFALVRKCRQGTGEYAAKFKIKRRSSSRGVSRRE 60
OY 61 IREVSILROVLHNVITLHDYENRTDVVHILEVSGELDFPLAOKESLSEEXTSFT 120
DB 61 IREVNILREIRHPNITLHDIFENKTDVLLLELVSGELDFLAEKESLSEEXTSFT 120
OY 121 KOILDGVNLTHTKKAHFDLKPENIMLDKNIPRIKIDFGLAHEIDEGVEFKNIFGT 180
DB 121 KOILDGVNLTHTKKAHFDLKPENIMLDKNVNPRIKIDFGIAHKIEAGNEFKNIFGT 180

DB 121 KOILDGVNLTHTKKAHFDLKPENIMLDKNVNPRIKIDFGIAHKIEAGNEFKNIFGT 180
OY 181 PEFVAPEIVNYEPLGLEADWMSIGVTYILLSGASPLGDTKQETLANTSYSDDEEF 240
DB 181 PEFVAPEIVNYEPLGLEADWMSIGVTYILLSGASPLGDTKQETLNTSAVYDDEEF 240
OY 241 FSHTSSELAKDFIRKLKLVKTRKRLTQDALRHPWITPV 278
DB 241 FSNITSELAKDFIRRLLVKDPKRRMTIAOSLEHSMIXPL 278

RESULT 11

US-09-724-676A-69504
;; Sequence 69504, Application US/09724676A
;; GENERAL INFORMATION:
;; APPLICANT: Compugen LTD
;; TITLE OF INVENTION: Variants of alternative splicing
;; FILE REFERENCE: 129181.4 Compugen
;; CURRENT APPLICATION NUMBER: US/09/724,676A
;; CURRENT FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 97222
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 69504
;; LENGTH: 282
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (276)..(276)
;; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-724-676A-69504

Query Match 62.9%; Score 1161; DB 5; Length 282;
Best Local Similarity 78.1%; Pred. No. 2.7e-97;
Matches 217; Conservative 39; Mismatches 22; Indels 0; Gaps 0;

OY 1 MEFPOKQKVEDFYDGEELGSGOFATVKKCREKSTGLEVAAFKIKKROASRGVSREE 60
DB 1 MSTFQEDVEDHDEYEMGEELGSGOFALVRKCRQGTGEYAAKFKIKRRSSSRGVSRRE 60
OY 61 IREVSILROVLHNVITLHDYENRTDVVHILEVSGELDFPLAOKESLSEEXTSFT 120
DB 61 IREVNILREIRHPNITLHDIFENKTDVLLLELVSGELDFPLAOKESLSEEXTSFT 120
OY 121 KOILDGVNLTHTKKAHFDLKPENIMLDKNIPRIKIDFGLAHEIDEGVEFKNIFGT 180
DB 121 KOILDGVNLTHTKKAHFDLKPENIMLDKNVNPRIKIDFGIAHKIEAGNEFKNIFGT 180
OY 181 PEFVAPEIVNYEPLGLEADWMSIGVTYILLSGASPLGDTKQETLANTSYSDDEEF 240
DB 181 PEFVAPEIVNYEPLGLEADWMSIGVTYILLSGASPLGDTKQETLNTSAVYDDEEF 240
OY 241 FSHTSSELAKDFIRKLKLVKTRKRLTQDALRHPWITPV 278
DB 241 FSNITSELAKDFIRRLLVKDPKRRMTIAOSLEHSMIXPL 278

RESULT 12

US-09-724-676-69506
;; Sequence 69506, Application US/09724676
;; GENERAL INFORMATION:
;; APPLICANT: Compugen LTD
;; TITLE OF INVENTION: Variants of alternative splicing
;; FILE REFERENCE: 129181.4 Compugen
;; CURRENT APPLICATION NUMBER: US/09/724,676
;; CURRENT FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 97222
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 69506
;; LENGTH: 595
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-724-676-69506


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0Y 59 EIEREVSILKOVHNN--VTTTHDYVNTDRVHLITELSGELP--FLAKESISE 114
Db 103 MEIHEIHLAVL-ELKODNRPWNLHEVYETJSEMLVETVAAAGEIFQOCVADEEAFKE 161
0Y 115 EATSFTRKOLLIDGVNLHTKRIANFDLAPENIMLMDKNIP1PHKILIDFGAHEIEGVF 174
Db 162 DVORLMROIEGVHFLTRTDVNVHLDLPQNMLTSES--PLGDIKIDVFGSLRKNSFL 220
0Y 175 KNIGTFPEVAPELVANEPLGSLADMSTGVITYILLSGASPLGOTKOTFLANTISVS 234
Db 221 REIMGTPEYAPELSLDPSMATDMMSIGVLYLMTLGTSPGLGNKOTFLNISOMNL 280
0Y 235 DDEEFPFSHSELAKDEIRKLIVETKRRRLTYOALRHPRTIVDNOAAVRESVYNDE 294
Db 281 SYSEEEFVLSAESAVDFRTRLVLYKPPEDRATAECCTKHPMLTQSSIOEPSEFRKALEEA 340
0Y 295 NFRQYVARRAKKLSFSTVSLCNHLTRLSMKVHLRPEDDLRKNESDPEEDIAARKAL 351
Db 341 N-----ALDGHGVSPEINSDTDSSEESIVTEELT 371

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Search completed: March 26, 2003, 19:17:03
Job time : 31.3146 secs

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QY 61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAOKESLSEEBATSFIKQILDGVNYLHT 120
| | | | |
DB 73 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAOKESLSEEBATSFIKQILDGVNYLHT 132
| | | | |
QY 121 KKAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVEFKNIFGTPFEVAPEIYVE 180
| | | | |
DB 133 KKAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVEFKNIFGTPFEVAPEIYVE 192
| | | | |
QY 181 PLGLEADWMSIGVITYILLSGASPFLGDTKQETLANITSVSYDDEEFFSHSTSELAQDFI 240
| | | | |
DB 193 PLGLEADWMSIGVITYILLSGASPFLGDTKQETLANITSVSYDDEEFFSHSTSELAQDFI 252
| | | | |
QY 241 RKLKVEKTRKRLTIOEALRHPWI 263
| | | | |
DB 253 RKLKVEKTRKRLTIOEALRHPWI 275
| | | | |

RESULT 2

PCT-US99-13411-2
; Sequence 2, Application PC/TUS9913411A
; GENERAL INFORMATION:
; APPLICANT: KIMCHI, Adl
; APPLICANT: MCINNIS A., Patricia
; APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
; FILE REFERENCE: KIMCHI2A
; CURRENT APPLICATION NUMBER: PCT/US99/13411A
; CURRENT FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,294
; EARLIER FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Human
PCT-US99-13411-2

Query Match 100.0%; Score 1343; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDIGEELSGGFATVKKCREKSTGLEAYAAKFIKKRSRASRGVSRREIEREVSILROYL 60
| | | | |
DB 13 YDIGEELSGGFATVKKCREKSTGLEAYAAKFIKKRSRASRGVSRREIEREVSILROYL 72
| | | | |
QY 61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAOKESLSEEBATSFIKQILDGVNYLHT 120
| | | | |
DB 73 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAOKESLSEEBATSFIKQILDGVNYLHT 132
| | | | |
QY 121 KKAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVEFKNIFGTPFEVAPEIYVE 180
| | | | |
DB 133 KKAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVEFKNIFGTPFEVAPEIYVE 192
| | | | |
QY 181 PLGLEADWMSIGVITYILLSGASPFLGDTKQETLANITSVSYDDEEFFSHSTSELAQDFI 240
| | | | |
DB 193 PLGLEADWMSIGVITYILLSGASPFLGDTKQETLANITSVSYDDEEFFSHSTSELAQDFI 252
| | | | |
QY 241 RKLKVEKTRKRLTIOEALRHPWI 263
| | | | |
DB 253 RKLKVEKTRKRLTIOEALRHPWI 275
| | | | |

RESULT 3
US-09-719-748-2

; Sequence 2, Application US/09719748
; GENERAL INFORMATION:
; APPLICANT: KIMCHI, Adl
; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
; FILE REFERENCE: KIMCHI2A
; CURRENT APPLICATION NUMBER: US/09/719,748
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/089,294

; PRIOR FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Human
US-09-719-748-2

Query Match 100.0%; Score 1343; DB 21; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDIGEELSGGFATVKKCREKSTGLEAYAAKFIKKRSRASRGVSRREIEREVSILROYL 60
| | | | |
DB 13 YDIGEELSGGFATVKKCREKSTGLEAYAAKFIKKRSRASRGVSRREIEREVSILROYL 72
| | | | |
QY 61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAOKESLSEEBATSFIKQILDGVNYLHT 120
| | | | |
DB 73 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAOKESLSEEBATSFIKQILDGVNYLHT 132
| | | | |
QY 121 KKAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVEFKNIFGTPFEVAPEIYVE 180
| | | | |
DB 133 KKAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVEFKNIFGTPFEVAPEIYVE 192
| | | | |
QY 181 PLGLEADWMSIGVITYILLSGASPFLGDTKQETLANITSVSYDDEEFFSHSTSELAQDFI 240
| | | | |
DB 193 PLGLEADWMSIGVITYILLSGASPFLGDTKQETLANITSVSYDDEEFFSHSTSELAQDFI 252
| | | | |
QY 241 RKLKVEKTRKRLTIOEALRHPWI 263
| | | | |
DB 253 RKLKVEKTRKRLTIOEALRHPWI 275
| | | | |

RESULT 4

US-09-791-537-13590
; Sequence 13590, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 13590
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-13590

Query Match 99.2%; Score 1332; DB 21; Length 370;
Best Local Similarity 99.6%; Pred. No. 9.3e-102;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDIGEELSGGFATVKKCREKSTGLEAYAAKFIKKRSRASRGVSRREIEREVSILROYL 60
| | | | |
DB 23 YDIGEELSGGFATVKKCREKSTGLEAYAAKFIKKRSRASRGVSRREIEREVSILROYL 82
| | | | |
QY 61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAOKESLSEEBATSFIKQILDGVNYLHT 120
| | | | |
DB 83 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAOKESLSEEBATSFIKQILDGVNYLHT 142
| | | | |
QY 121 KKAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVEFKNIFGTPFEVAPEIYVE 180
| | | | |
DB 143 KKAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVEFKNIFGTPFEVAPEIYVE 202
| | | | |
QY 181 PLGLEADWMSIGVITYILLSGASPFLGDTKQETLANITSVSYDDEEFFSHSTSELAQDFI 240
| | | | |
DB 203 PLGLEADWMSIGVITYILLSGASPFLGDTKQETLANITSVSYDDEEFFSHSTSELAQDFI 262
| | | | |

QY 241 RKLIVKTRKRLTIOEALRHPWI 263
Db 263 RKLIVKTRKRLTIOEALRHPWI 285

RESULT 5

US-09-791-537-108109
; Sequence 108109, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Dancer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108109
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-108109

Query Match 98.4%; Score 1321; DB 21; Length 370;
Best Local Similarity 98.9%; Pred. No. 7, 6e-101;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDIGEELSGGQFAIVKCKREKSTGLEAYAKFKIKKRSRASRGVSREIEREVSILROYL 60
Db 23 YDIGEELSGGQFAIVKCKREKSTGLEAYAKFKIKKRSRASRGVSREIEREVSILROYL 82
QY 61 HHNVITLHDYENRTDVVHILELVSGGELFDFLAOKESLSEEAATSFIKOILDGVNVLHT 120
Db 83 HHNVITLHDYENRTDVVHILELVSGGELFDFLAOKESLSEEAATSFIKOILDGVNVLHT 142
QY 121 KRIAHFDLKPENIMLDKNIPRIPIKILDFGLAHIEDGVEFNINIGTPEFVAPEIYNYE 180
Db 143 KRIAHFDLKPENIMLDKNIPRIPIKILDFGLAHIEDGVEFNINIGTPEFVAPEIYNYE 202
QY 181 PGLLEADMSIGVITYILLSGASPFGLDGTKEOTLANITSVSYDDEEFFSHTSELAOKDFI 240
Db 203 PGLLEADMSIGVITYILLSGASPFGLDGTKEOTLANITAVSYDDEEFFSHTSELAOKDFI 262
QY 241 RKLIVKTRKRLTIOEALRHPWI 263
Db 263 RKLIVKTRKRLTIOEALRHPWI 285

RESULT 6

US-09-791-537-108110
; Sequence 108110, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Dancer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108110
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-108110

Query Match 96.6%; Score 1297; DB 21; Length 370;
Best Local Similarity 97.3%; Pred. No. 7, 4e-99;

Matches 256; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YDIGEELSGGQFAIVKCKREKSTGLEAYAKFKIKKRSRASRGVSREIEREVSILROYL 60
Db 23 YDIGEELSGGQFAIVKCKREKSTGLEAYAKFKIKKRSRASRGVSREIEREVSILROYL 82
QY 61 HHNVITLHDYENRTDVVHILELVSGGELFDFLAOKESLSEEAATSFIKOILDGVNVLHT 120
Db 83 HHNVITLHDYENRTDVVHILELVSGGELFDFLAOKESLSEEAATSFIKOILDGVNVLHT 142
QY 121 KRIAHFDLKPENIMLDKNIPRIPIKILDFGLAHIEDGVEFNINIGTPEFVAPEIYNYE 180
Db 143 KRIAHFDLKPENIMLDKNIPRIPIKILDFGLAHIEDGVEFNINIGTPEFVAPEIYNYE 202
QY 181 PGLLEADMSIGVITYILLSGASPFGLDGTKEOTLANITSVSYDDEEFFSHTSELAOKDFI 240
Db 203 PGLLEADMSIGVITYILLSGASPFGLDGTKEOTLANITAVSYDDEEFFSHTSELAOKDFI 262
QY 241 RKLIVKTRKRLTIOEALRHPWI 263
Db 263 RKLIVKTRKRLTIOEALRHPWI 285

RESULT 7

PCT-US01-08631-39633
; Sequence 39633, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39633
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (128)..(147)
; OTHER INFORMATION: TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE domain identified
; OTHER INFORMATION: by EMATRIX, accession number PR00109B, p-value=7.055e-11, raw
; NAME/KEY: DOMAIN
; LOCATION: (20)..(274)
; OTHER INFORMATION: Eukaryotic protein kinase domain identified by Pfam,
; OTHER INFORMATION: accession name pkinase, E-value=3.9e-76, Pfam score of 266.3
PCT-US01-08631-39633

Query Match 95.2%; Score 1278; DB 1; Length 359;

Best Local Similarity 98.8%; Pred. No. 2, 7e-97;
Matches 252; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 SCQFAIVKCKREKSTGLEAYAKFKIKKRSRASRGVSREIEREVSILROYLHHNVITLH 68
Db 20 SCQFAIVKCKREKSTGLEAYAKFKIKKRSRASRGVSREIEREVSILROYLHHNVITLH 79
QY 69 DYVENRTDVVHILELVSGGELFDFLAOKESLSEEAATSFIKOILDGVNVLHTKRIAHFDL 128
Db 80 DYVENRTDVVHILELVSGGELFDFLAOKESLSEEAATSFIKOILDGVNVLHTKRIAHFDL 139
QY 129 KPEINIMLDKNIPRIPIKILDFGLAHIEDGVEFNINIGTPEFVAPEIYNYEPLGLEADM 188
Db 140 KPEINIMLDKNIPRIPIKILDFGLAHIEDGVEFNINIGTPEFVAPEIYNYEPLGLEADM 199
QY 189 WSIGVITYILLSGASPFGLDGTKEOTLANITSVSYDDEEFFSHTSELAOKFKRLVKEK 248
Db 200 WSIGVITYILLSGASPFGLDGTKEOTLANITAVSYDDEEFFSHTSELAOKFKRLVKEK 259

OY 249 RKLRTIOEALRHPWI 263
Db 260 RRLVTKDPRKMTIODSLQHPWI 274

RESULT 8
PCT-US99-13411-3
Sequence 3, Application PC/TUS9913411

GENERAL INFORMATION:
APPLICANT: KIMCHI, Adl

APPLICANT: MCINNIS A., Patricia

APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.

TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN

FILE REFERENCE: KIMCHI2A

CURRENT FILING DATE: 1999-06-15

EARLIER FILING DATE: 1998-06-15

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 263

TYPE: PRT

ORGANISM: Human

PCT-US99-13411-3

Query Match

Best Local Similarity 83.7%; Score 1124; DB 1; Length 263;

Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

OY 1 YDIGEELGSGQFAIVKCKREKSTGLEVAAKFTKKROSRRGVSREELEREVSILROYL 60

Db 1 YDIGEELGSGQFAIVKCKREKSTGLEVAAKFTKKRRTKSRGVSREELEREVSILKEIQ 60

OY 61 HHNVITLHDYENKRTDVNHLLELVSGGELFDFLAOKESLSEEAATSFIKQILDGVNYLHT 120

Db 61 HPNVITLHEVEYENKRTDVILLELVAGGELFDFLAOKESLSEEAATSFELKQILNGVYLYHS 120

OY 121 KRIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHEIDGVEFNKIFGTFEFAPELVAYNE 180

Db 121 LOIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHKIDFENFNKIFGTFEFAPELVAYNE 180

OY 181 PLGLEADWMSIGVITYTLLSGASPLGDTKQETLANITSVSYDFDEEFSHTSELAKDFT 240

Db 181 PLGLEADWMSIGVITYTLLSGASPLGDTKQETLANITSVSYDFDEEFSHTSELAKDFT 240

OY 241 RKLIVKTRKRLTIOEALRHPWI 263

Db 241 RRLVTKDPRKMTIODSLQHPWI 263

RESULT 9
PCT-US99-13411-3
Sequence 3, Application PC/TUS9913411A

GENERAL INFORMATION:
APPLICANT: KIMCHI, Adl

APPLICANT: MCINNIS A., Patricia

APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.

TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN

FILE REFERENCE: KIMCHI2A

CURRENT FILING DATE: 1999-06-15

EARLIER FILING DATE: 1998-06-15

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 263

TYPE: PRT

ORGANISM: Human

PCT-US99-13411-3

Query Match

Best Local Similarity 83.7%; Score 1124; DB 1; Length 263;

Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

OY 1 YDIGEELGSGQFAIVKCKREKSTGLEVAAKFTKKROSRRGVSREELEREVSILROYL 60

Db 1 YDIGEELGSGQFAIVKCKREKSTGLEVAAKFTKKRRTKSRGVSREELEREVSILKEIQ 60

OY 61 HHNVITLHDYENKRTDVNHLLELVSGGELFDFLAOKESLSEEAATSFIKQILDGVNYLHT 120

Db 61 HPNVITLHEVEYENKRTDVILLELVAGGELFDFLAOKESLSEEAATSFELKQILNGVYLYHS 120

OY 121 KRIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHEIDGVEFNKIFGTFEFAPELVAYNE 180

Db 121 LOIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHKIDFENFNKIFGTFEFAPELVAYNE 180

OY 181 PLGLEADWMSIGVITYTLLSGASPLGDTKQETLANITSVSYDFDEEFSHTSELAKDFT 240

Db 181 PLGLEADWMSIGVITYTLLSGASPLGDTKQETLANITSVSYDFDEEFSHTSELAKDFT 240

OY 241 RKLIVKTRKRLTIOEALRHPWI 263

Db 241 RRLVTKDPRKMTIODSLQHPWI 263

RESULT 10
US-09-719-748-3
Sequence 3, Application US/09719748

GENERAL INFORMATION:
APPLICANT: KIMCHI, Adl

APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.

TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN

FILE REFERENCE: KIMCHI2A

CURRENT FILING DATE: 2000-12-15

PRIOR APPLICATION NUMBER: 60/089,294

PRIOR FILING DATE: 1998-06-15

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 263

TYPE: PRT

ORGANISM: Human

US-09-719-748-3

Query Match

Best Local Similarity 83.7%; Score 1124; DB 21; Length 263;

Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

OY 1 YDIGEELGSGQFAIVKCKREKSTGLEVAAKFTKKROSRRGVSREELEREVSILROYL 60

Db 1 YDIGEELGSGQFAIVKCKREKSTGLEVAAKFTKKRRTKSRGVSREELEREVSILKEIQ 60

OY 61 HHNVITLHDYENKRTDVNHLLELVSGGELFDFLAOKESLSEEAATSFIKQILDGVNYLHT 120

Db 61 HPNVITLHEVEYENKRTDVILLELVAGGELFDFLAOKESLSEEAATSFELKQILNGVYLYHS 120

OY 121 KRIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHEIDGVEFNKIFGTFEFAPELVAYNE 180

Db 121 LOIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHKIDFENFNKIFGTFEFAPELVAYNE 180

OY 181 PLGLEADWMSIGVITYTLLSGASPLGDTKQETLANITSVSYDFDEEFSHTSELAKDFT 240

Db 181 PLGLEADWMSIGVITYTLLSGASPLGDTKQETLANITSVSYDFDEEFSHTSELAKDFT 240

OY 241 RKLIVKTRKRLTIOEALRHPWI 263

Db 241 RRLVTKDPRKMTIODSLQHPWI 263

RESULT 11
US-09-538-092-1198
Sequence 1198, Application US/09538092

GENERAL INFORMATION:

APPLICANT: Gluc, Lolo
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538, 092
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormat Version 0.9
SEQ ID NO 1198
LENGTH: 1431
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P53355
US-09-538-092-1198

Query Match 83.7%; Score 1124; DB 19; Length 1431;
Best Local Similarity 79.5%; Pred. No. 9,8e-84;
Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

QY 1 YDIGELSGGQFAIVKCKREKSTGLEVAAKFKRKRSRGRVSGREIEEVSILKEIO 60
DB 13 YDTGELSGGQFAIVKCKREKSTGLEVAAKFKRKRTSSRGVSGREIEEVSILKEIO 72
QY 61 HHNVITLHDVYENRDVHILEVSGELDFDLAOKESLSEBATSFIKQILDGVNYLHT 120
DB 73 HHNVITLHDVYENRDVHILEVSGELDFDLAOKESLSEBATSFIKQILDGVNYLHT 132
QY 121 KKAHFDLKPENIMLLDKNIPRIKILDFGLAHEIDGVEKRNIFGTPEFAPELVNTE 180
DB 133 LQIAHFDLKPENIMLLDKNIPRIKILDFGLAHEIDGVEKRNIFGTPEFAPELVNTE 192
QY 181 PLGLEADMSISGIVTYILLSGASPLGDTKQETLANITSVSDPDEEFSHTSELAKEFI 240
DB 193 PLGLEADMSISGIVTYILLSGASPLGDTKQETLANITSVSDPDEEFSHTSELAKEFI 252
QY 241 RKLKVEKTRKRLTIQDALRHPWI 263
DB 253 RRLVYDKPKRMTIDPSLOHPWI 275

RESULT 12
US-09-791-537-49880
Sequence 49880, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomolx, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 49880
LENGTH: 1431
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-49880

Query Match 83.7%; Score 1124; DB 21; Length 1431;
Best Local Similarity 79.5%; Pred. No. 9,8e-84;
Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;
QY 1 YDIGELSGGQFAIVKCKREKSTGLEVAAKFKRKRSRGRVSGREIEEVSILKEIO 60
DB 13 YDTGELSGGQFAIVKCKREKSTGLEVAAKFKRKRTSSRGVSGREIEEVSILKEIO 72

DB 13 YDTGELSGGQFAIVKCKREKSTGLEVAAKFKRKRTSSRGVSGREIEEVSILKEIO 72
QY 61 HHNVITLHDVYENRDVHILEVSGELDFDLAOKESLSEBATSFIKQILDGVNYLHT 120
DB 73 HHNVITLHDVYENRDVHILEVSGELDFDLAOKESLSEBATSFIKQILDGVNYLHT 132
QY 121 KKAHFDLKPENIMLLDKNIPRIKILDFGLAHEIDGVEKRNIFGTPEFAPELVNTE 180
DB 133 LQIAHFDLKPENIMLLDKNIPRIKILDFGLAHEIDGVEKRNIFGTPEFAPELVNTE 192
QY 181 PLGLEADMSISGIVTYILLSGASPLGDTKQETLANITSVSDPDEEFSHTSELAKEFI 240
DB 193 PLGLEADMSISGIVTYILLSGASPLGDTKQETLANITSVSDPDEEFSHTSELAKEFI 252
QY 241 RKLKVEKTRKRLTIQDALRHPWI 263
DB 253 RRLVYDKPKRMTIDPSLOHPWI 275

RESULT 13
US-60-350-061-273
Sequence 273, Application US/60350061
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS T
FILE REFERENCE: D0185
CURRENT APPLICATION NUMBER: US/60/350,061
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 981
SOFTWARE: PatentIn version 3.0
SEQ ID NO 273
LENGTH: 1431
TYPE: PRT
ORGANISM: Homo sapiens
US-60-350-061-273

Query Match 83.7%; Score 1124; DB 27; Length 1431;
Best Local Similarity 79.5%; Pred. No. 9,8e-84;
Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;
QY 1 YDIGELSGGQFAIVKCKREKSTGLEVAAKFKRKRSRGRVSGREIEEVSILKEIO 60
DB 13 YDTGELSGGQFAIVKCKREKSTGLEVAAKFKRKRTSSRGVSGREIEEVSILKEIO 72
QY 61 HHNVITLHDVYENRDVHILEVSGELDFDLAOKESLSEBATSFIKQILDGVNYLHT 120
DB 73 HHNVITLHDVYENRDVHILEVSGELDFDLAOKESLSEBATSFIKQILDGVNYLHT 132
QY 121 KKAHFDLKPENIMLLDKNIPRIKILDFGLAHEIDGVEKRNIFGTPEFAPELVNTE 180
DB 133 LQIAHFDLKPENIMLLDKNIPRIKILDFGLAHEIDGVEKRNIFGTPEFAPELVNTE 192
QY 181 PLGLEADMSISGIVTYILLSGASPLGDTKQETLANITSVSDPDEEFSHTSELAKEFI 240
DB 193 PLGLEADMSISGIVTYILLSGASPLGDTKQETLANITSVSDPDEEFSHTSELAKEFI 252
QY 241 RKLKVEKTRKRLTIQDALRHPWI 263
DB 253 RRLVYDKPKRMTIDPSLOHPWI 275

RESULT 14
US-60-375-626-6
Sequence 6, Application US/60375626
GENERAL INFORMATION:
APPLICANT: Weich, Nadine
TITLE OF INVENTION: Methods and compositions for treating
FILE REFERENCE: MP102-063P1(m)
CURRENT APPLICATION NUMBER: US/60/375,626
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1431
; TYPE: PRT
; ORGANISM: Homosapien
us-60-375-626-6

Query Match 83.7%; Score 1124; DB 27; Length 1431;
Best Local Similarity 79.5%; Pred. No. 9,8e-84;
Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

QY 1 YDIGEELSGGQFAIVKCKREKSTGLEVAKPFKKRQSRASRGVSRREIEREVSILRQVL 60
|||
DB 13 YDTGEBLSSGGQFAVKKCKREKSTGLQYAAKFKKKRRTSSRRGVSRREDIEREVSILKEIQ 72
QY 61 HHNVITLHDVYENKRDVYHILELVSGGELFDELQAKESLSEEPATSFIKQILDGVNYLHT 120
|
DB 73 HPNVITLHEVYENKRDVYHILELVAGGELFDELQAKESLSEEPATSFIKQILDGVNYLHTS 132
QY 121 KRIAFDLKPEINIMLDKNIPPIPIKILDFGLAHEIEDGVFEKNIFGTPEFVAPETVNYE 180
:
DB 133 LQIAHFDLKPENIMLDKNVPRKRIKIDFGIAHKIDFGNEKNIFGTPEFVAPETVNYE 192
QY 181 PLGLEADWMSIGVITYILLSGASPFGLDTKQETLANITSVSYDFDEEFFSHTSSELAQDFI 240
|||
DB 193 PLGLEADWMSIGVITYILLSGASPFGLDTKQETLANIVSAVNYEDEFYFNTSALAKDFI 252
QY 241 RKLVKETRRKRLTIOEALRHPWI 263
|
DB 253 RRLVKDPPKRRMTIAQSLHSHWI 275
|

RESULT 15

US-09-719-748-4
; Sequence 4, Application US/09719748
; GENERAL INFORMATION:
; APPLICANT: KIMCHI, Adi
; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
; FILE REFERENCE: KIMCHI2A
; CURRENT APPLICATION NUMBER: US/09/719,748
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/089,294
; PRIOR FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Human
US-09-719-748-4

Query Match 83.5%; Score 1121; DB 21; Length 263;
Best Local Similarity 79.8%; Pred. No. 1.9e-84;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

QY 1 YDIGEELSGGQFAIVKCKREKSTGLEVAKPFKKRQSRASRGVSRREIEREVSILRQVL 60
|
DB 1 YEMGEELSGGQFAIVKCKRKQCTGKKEYAKFTKKRRLSSRRGVSRREIEREVSILREIR 60
QY 61 HHNVITLHDVYENKRDVYHILELVSGGELFDELQAKESLSEEPATSFIKQILDGVNYLHT 120
|
DB 61 HPNVITLHEVYENKRDVYHILELVSGGELFDELQAKESLSEEPATSFIKQILDGVNYLHTS 120
QY 121 KRIAFDLKPEINIMLDKNIPPIPIKILDFGLAHEIEDGVFEKNIFGTPEFVAPETVNYE 180
|
DB 121 KRIAFDLKPEINIMLDKNVPRKRIKIDFGIAHKIDFGNEKNIFGTPEFVAPETVNYE 180
QY 181 PLGLEADWMSIGVITYILLSGASPFGLDTKQETLANITSVSYDFDEEFFSHTSSELAQDFI 240
|||
DB 181 PLGLEADWMSIGVITYILLSGASPFGLDTKQETLANISAVNYEDEFYFNTSALAKDFI 240
QY 241 RKLVKETRRKRLTIOEALRHPWI 263
|

DB 241 RRLVKDPPKRRMTIAQSLHSHWI 263

Search completed: March 26, 2003, 19:16:09
Job time : 119.936 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:09:46 : Search time 20.6854 Seconds
(without alignments)
1678.167 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343
Sequence: 1 YDIGEELSGGFATVKKRCRE.....LVKTRKRRLTIOEALRHPWI 263

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 613006 seqs, 131990659 residues

Total number of hits satisfying chosen parameters: 613006

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/plodata/1/paa/PC/CT_NEW_COMB.pep:*
2: /cgn2_6/plodata/1/paa/US03_NEW_COMB.pep:*
3: /cgn2_6/plodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/plodata/1/paa/US08_NEW_COMB.pep:*
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7: /cgn2_6/plodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	98.4	370	7	US-60-443-566-3011 Sequence 3011, App
2	1124	83.7	1431	1	PC/CT-US03-02484-38 Sequence 38, Appl
3	1124	83.7	1431	5	US-09-949-002-377 Sequence 37, App
4	1124	83.7	1431	6	US-10-348-119-220 Sequence 220, App
5	1124	83.7	1436	7	US-60-443-566-4055 Sequence 4055, App
6	1121	83.5	282	5	US-09-724-676-69504 Sequence 69504, A
7	1121	83.5	282	5	US-09-724-676A-69504 Sequence 69504, A
8	1121	83.5	454	6	PC/CT-US02-31357-119 Sequence 119, App
9	1121	83.5	454	6	US-10-262-445-119 Sequence 119, App
10	1121	83.5	454	7	US-60-443-566-2831 Sequence 2831, App
11	1121	83.5	595	5	US-09-724-676-69506 Sequence 69506, A
12	1121	83.5	595	5	US-09-949-002-486 Sequence 486, App
13	1087	80.9	1412	5	US-09-949-002-486 Sequence 6344, App
14	660.5	49.2	2783	6	US-60-443-566-2540 Sequence 2540, App
15	638	47.5	298	4	US-10-274-978-18 Sequence 18, Appl
16	636.5	47.4	508	6	US-10-274-978-19 Sequence 19, Appl
17	636.5	47.4	508	6	US-60-443-566-2980 Sequence 2980, App
18	625	46.5	596	7	US-10-311-034-6 Sequence 6, Appl
19	540.5	40.2	514	3	US-10-258-106-11 Sequence 11, Appl
20	514	38.3	355	6	US-10-355-975-10 Sequence 10, Appl
21	514	38.3	355	6	US-10-258-106-2 Sequence 2, Appl
22	514	38.3	357	6	US-60-435-108-2 Sequence 2, Appl
23	514	38.3	357	7	PC/CT-US02-40194-15 Sequence 15, Appl
24	509	37.9	473	6	US-10-320-351-15 Sequence 15, Appl
25	509	37.9	473	6	US-10-274-978-15 Sequence 15, Appl
26	500	37.2	274	6	US-10-274-978-15 Sequence 15, Appl

27	500	37.2	414	6	US-10-274-978-14 Sequence 14, Appl
28	500	37.2	460	7	US-60-443-566-3356 Sequence 3356, App
29	500	37.2	476	7	US-60-443-566-3355 Sequence 3355, App
30	500	37.2	2861	1	PC/CT-US02-14877A-687 Sequence 687, App
31	500	37.2	2861	6	US-10-240-851-108 Sequence 108, App
32	500	37.2	2861	6	US-10-099-056-1370 Sequence 1370, App
33	500	37.2	3038	6	US-10-274-978-26 Sequence 26, Appl
34	492.5	36.7	549	16	US-10-274-978-6 Sequence 6, Appl
35	492.5	36.7	846	6	US-10-274-978-4 Sequence 4, Appl
36	492.5	36.7	2380	6	US-10-333-314-18 Sequence 18, Appl
37	492.5	36.7	3267	1	PC/CT-US02-33723-28 Sequence 28, Appl
38	488.5	36.4	256	6	US-10-072-012-799 Sequence 799, App
39	488.5	36.4	256	6	US-10-072-012-856 Sequence 856, App
40	488.5	36.4	256	6	US-10-072-012-876 Sequence 876, App
41	488.5	36.4	256	6	US-10-072-012-882 Sequence 882, App
42	488	36.3	499	1	PC/CT-US03-02588-88 Sequence 88, Appl
43	488	36.3	499	6	US-10-354-358-88 Sequence 88, Appl
44	488	36.3	533	6	US-10-160-619-176 Sequence 176, App
45	487.5	36.3	254	6	US-10-074-978A-150 Sequence 150, App

ALIGNMENTS

RESULT 1
US-60-443-566-3011
Sequence 3011, Application US/60443566
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001447
CURRENT APPLICATION NUMBER: US/60/443,566
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 25102
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3011
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-60-443-566-3011

Query Match 98.4%; Score 1321; DB 7; Length 370;
Best Local Similarity 98.9%; Pred. No. 3.6e-120;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDIGEELSGGFATVKKRCREKSTGLFYAAKFKRKQSRASRGVSRREIEREVSILRQVL 60
Sequence 3011, Appl
DB 23 YDIGEELSGGFATVKKRCREKSTGLFYAAKFKRKQSRASRGVSRREIEREVSILRQVL 82
Sequence 38, Appl

QY 61 HHNVITLHDVYENRFTDVVHILELVSGGELDFDLAQKESLSEEAATSTFKOILDGVTLYHT 120
Sequence 220, App
DB 83 HHNVITLHDVYENRFTDVVHILELVSGGELDFDLAQKESLSEEAATSTFKOILDGVTLYHT 142
Sequence 4055, App

QY 121 KTAHPLKPEKNTMLDKNIPPIKILIDGLAHEIDVGEFKIKFTPTPEVAEINYE 180
Sequence 119, App
DB 143 KTAHPLKPEKNTMLDKNIPPIKILIDGLAHEIDVGEFKIKFTPTPEVAEINYE 202
Sequence 69504, A

QY 181 PLGLEAMMSIGVTTIYLLSGASPLDGTQOETLANITSSYDDEFFSFTSLANDFI 240
Sequence 486, App
DB 203 PLGLEAMMSIGVTTIYLLSGASPLDGTQOETLANITSSYDDEFFSFTSLANDFI 262
Sequence 6344, App

QY 241 RKLIVKTRKRRLTIOEALRHPWI 263
Sequence 2540, App
DB 263 RKLIVKTRKRRLTIOEALRHPWI 285
Sequence 2, Appl

RESULT 2
PC/CT-US03-02484-38
Sequence 38, Application PC/CTUS0302484
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.

APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Aileen
APPLICANT: Welch, Nadine S.
APPLICANT: Kelly, Louise M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 189, 12303, 13906,
TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
FILE REFERENCE: MP102-019
CURRENT APPLICATION NUMBER: PCT/US03/02484
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/354,333
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 60/360,258
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/364,476
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/375,626
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/386,494
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/390,965
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: US 60/392,480
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/394,128
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/399,783
PRIOR FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US 60/403,221
PRIOR FILING DATE: 2002-08-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 1431
TYPE: PRT
ORGANISM: Homo Sapiens
PCT-US03-02484-38

```

Query Match      83.7%; Score 1124; DB 1; Length 1431;
Best Local Similarity 79.5%; Pred. No.3.9e-100;
Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

QY      1 YDGEELSGSQFAIVKCKREKSTGLEEYAAFKIKKQSRASRGRVSGREELEREVSILKQVL 60
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd      13 YDTGEEGSGGFAVKKCKREKSTGLGYAAFKIKRKRRKSSRRGSRDDIEREVSILKEIQ 72
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      61 HHNVITLHDVYENTDVVHILELVSGGELDFDLAOKESLSSEETSFITKOLLDOVNI LHT 120
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd      73 HPNVITLHEVENKTDVILILEVAGGELDFLAKESLTFEEETFEFLKOLLNIVYLLHS 132
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      121 KRIAHFDLKPENIMLDRNIPRPIKILIDGLAHEIEDGYEENKIFGTPPEFAVEIYNE 180
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd      133 LQIAHFDLKPENIMLDRNVPKPRIKIIDFLAKHIFGNEFNKIFGTPPEFAVEIYNE 192
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      181 PLGAEADWMSGCVITYIILSGASPFELGDTKQETLANITSVYDDEDEEFSHTSLANDFI 240
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd      193 PLGAEADWMSIGVITYIILSGASPFELGDTKQETLANISAVNEEDEFESNTSALAKDEI 252
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      241 RKLAVKETRRKRLTIOEALRHPWI 263
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd      253 RRLVTKDPKKRMWTIODSLQHPWI 275
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-09-949-002-377
; Sequence 377. Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

```

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: TITLE REFERENCE: AND USES THEREOF
: FILE REFERENCE: C1000790
: CURRENT APPLICATION NUMBER: US/09/949,002
: CURRENT FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: 60/231,401
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 10823
: SOFTWARE: RESLSEQ for Windows Version 4.0
: SEQ ID NO: 377
: LENGTH: 1431
: TYPE: PRT
: ORGANISM: Human
: OS-09-949-002-377

```

[illegible]

```

RESULT 4
US-10-348-119-ZZ0
; Sequence 220. Application US/10348119
GENERAL INFORMATION:
APPLICANT: Bristol Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND PEPTIDE FOR PREDICTING TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE PATHWAYS
FILE REFERENCE: D0185 NP
CURRENT APPLICATION NUMBER: US/10/348.119
PRIORITY FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: US 60/350,061
NUMBER OF SEQ ID NOS: 795
SOFTWARE: PatentIn version 3.2
SEQ ID NO 220
LENGTH: 1431
TYPE: PRF
ORGANISM: Homo sapiens
US-10-348-119-220

Query Match      83.7%   Score 1124; DB 6; Length 1431;
Best Local Similarity 79.5%; Pred No. 3,9e+100;
Matches 209; Conservative 41; Mismatches 11; Indels 0; Gaps 0;
```


Db 253 RRLVADPKRRMTIAOSLEHSMI 275

RESULT 10

US-60-443-566-2831
: Sequence 2831, Application US/60443566
: GENERAL INFORMATION:
: APPLICANT: CARCILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01447
: CURRENT APPLICATION NUMBER: US/60/443,566
: CURRENT FILING DATE: 2003-01-30
: NUMBER OF SEQ ID NOS: 25102
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 2831
: LENGTH: 454
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-443-566-2831

Query Match 83.5%; Score 1121; DB 7; Length 454;
Best Local Similarity 79.8%; Pred. No. 1.3e-100;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDIGELSGGQFAIVKCKREKSTGLEAYAKFTIKKROSASRGVSRREIEREVSILROYL 60
Db 13 YEMGELSGGQFAIVKCKQKGTGKEYAKFTIKRRSSRGVSRREIEREVNILLREIR 72
Qy 61 HHNVITLHDVYENRDTDVVHILELVSGGELDFDLAOKESISEEPAATFQKQILDGVNYLHT 120
Db 73 HPNITLHDIFENKTDVVLILELVSGGELDFDLAOKESLTEDAATQFLKQILDGVNYLHTS 132
Qy 121 KRIAHFDLKPENIMLDKNIPPIPIKIDFGLAHEIEDGVEFNKIFGTPEFVAPELVNVE 180
Db 133 KRIAHFDLKPENIMLDKNVNPRIKIDFGIAHKEAGNEFNKIFGTPEFVAPELVNVE 192
Qy 181 PGLGADWMSIGVITYILLSGASPLGDTKQETLANITSVSVDFDEFFSHTSELAKDFT 240
Db 193 PGLGADWMSIGVITYILLSGASPLGDTKQETLANISAVNYDFDEFFSHTSELAKDFT 252
Qy 241 RKLVEKTRKRLTIOEARHPMT 263
Db 253 RRLVADPKRRMTIAOSLEHSMI 275

RESULT 11

US-09-724-676-69506
: Sequence 69506, Application US/09724676
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 69506
: LENGTH: 595
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-724-676-69506

Query Match 83.5%; Score 1121; DB 5; Length 595;
Best Local Similarity 79.8%; Pred. No. 2e-100;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDIGELSGGQFAIVKCKREKSTGLEAYAKFTIKKROSASRGVSRREIEREVSILROYL 60
Db 13 YEMGELSGGQFAIVKCKQKGTGKEYAKFTIKRRSSRGVSRREIEREVNILLREIR 72

Qy 61 HHNVITLHDVYENRDTDVVHILELVSGGELDFDLAOKESISEEPAATFQKQILDGVNYLHT 120
Db 73 HPNITLHDIFENKTDVVLILELVSGGELDFDLAOKESLTEDAATQFLKQILDGVNYLHTS 132
Qy 121 KRIAHFDLKPENIMLDKNIPPIPIKIDFGLAHEIEDGVEFNKIFGTPEFVAPELVNVE 180
Db 133 KRIAHFDLKPENIMLDKNVNPRIKIDFGIAHKEAGNEFNKIFGTPEFVAPELVNVE 192
Qy 181 PGLGADWMSIGVITYILLSGASPLGDTKQETLANITSVSVDFDEFFSHTSELAKDFT 240
Db 193 PGLGADWMSIGVITYILLSGASPLGDTKQETLANISAVNYDFDEFFSHTSELAKDFT 252
Qy 241 RKLVEKTRKRLTIOEARHPMT 263
Db 253 RRLVADPKRRMTIAOSLEHSMI 275

RESULT 12

US-09-724-676A-69506
: Sequence 69506, Application US/09724676A
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676A
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 69506
: LENGTH: 595
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-724-676A-69506

Query Match 83.5%; Score 1121; DB 5; Length 595;
Best Local Similarity 79.8%; Pred. No. 2e-100;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDIGELSGGQFAIVKCKREKSTGLEAYAKFTIKKROSASRGVSRREIEREVSILROYL 60
Db 13 YEMGELSGGQFAIVKCKQKGTGKEYAKFTIKRRSSRGVSRREIEREVNILLREIR 72
Qy 61 HHNVITLHDVYENRDTDVVHILELVSGGELDFDLAOKESISEEPAATFQKQILDGVNYLHT 120
Db 73 HPNITLHDIFENKTDVVLILELVSGGELDFDLAOKESLTEDAATQFLKQILDGVNYLHTS 132
Qy 121 KRIAHFDLKPENIMLDKNIPPIPIKIDFGLAHEIEDGVEFNKIFGTPEFVAPELVNVE 180
Db 133 KRIAHFDLKPENIMLDKNVNPRIKIDFGIAHKEAGNEFNKIFGTPEFVAPELVNVE 192
Qy 181 PGLGADWMSIGVITYILLSGASPLGDTKQETLANITSVSVDFDEFFSHTSELAKDFT 240
Db 193 PGLGADWMSIGVITYILLSGASPLGDTKQETLANISAVNYDFDEFFSHTSELAKDFT 252
Qy 241 RKLVEKTRKRLTIOEARHPMT 263
Db 253 RRLVADPKRRMTIAOSLEHSMI 275

RESULT 13

US-09-948-002-486
: Sequence 486, Application US/09948002
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CLO00790
: CURRENT APPLICATION NUMBER: US/09/949,002
: CURRENT FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: 60/231,401
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 10823

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 486
; LENGTH: 1412
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-486

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```

Query Match      80.9%; Score 1087; DB 5; Length 1412;
Best Local Similarity 79.0%; Pred. No. 1.5e-96;
Matches 203; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

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OY 7 LGSQGFAYKKCREKSTGLEVAAKFIKKRQSRASRGVSREREVSILROYLHNHVT 66
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 LFSQFAVKKCKREKSTLOYAAKFIKKRKRKSSRGSRDIEREVSILKEIGHNVT 60
OY 67 LHAYENFTDVHILEVSGGELFDEFLAQKESLSEBEATSTIKOILDGVNLTHTKIAHF 126
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LHEVENKTQVILILEVAGGELFDEFLAEKESLSEBEATEFKOILNGVYLHSIQIAHF 120
OY 127 DLKPENIMLLDKNIPPIPHIKLIDFGLAHEIDGVEFKNIFGTPPEVAPEIYNVEPLGEA 186
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 DLKPENIMLLBRNVPKPKIKIIDFGLAHKIDFGNEFKNIFGTPPEVAPEIYNVEPLGEA 180
OY 187 DMSIGVITYILLSGASPLGDTKQETLANITSVSYDFEEFHSHTSELANDFTIRKLLVK 246
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 DMSIGVITYILLSGASPLGDTKQETLANITSVSYDFEEFHSHTSELANDFTIRKLLVK 240
OY 247 ETRKRLTQOALRHPWI 263
    :|||||:|||||
DB 241 DPKRRMTQDSLDHPWI 257

```

RESULT 14

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US-10-369-493-6344
; Sequence 6344, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369, 493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360, 039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6344
; LENGTH: 2783
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6344

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Query Match      49.2%; Score 660.5; DB 6; Length 2783;
Best Local Similarity 47.3%; Pred. No. 1.2e-54;
Matches 125; Conservative 61; Mismatches 69; Indels 9; Gaps 3;

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OY 1 YDGEELSGQFAIVKKCREKSTGLEVAAKFIKKRQSRASRGVSREREVSILROYL 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 195 YTIHEELGAGATYVIRATEKATGKTMAKKVQVR-----GVKKENVYIHEISMNQHL 248
OY 61 HHNVITLHDVYENRQDVHILEVSGGELFDEFLAQKESL-SEBEATSTIKOILDGVNLT 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 249 HEKLTNLHFAFMGNMWMLEEVSGGELFEKILDDSLMSEEDVDYHQIILLGVSHMH 308
OY 120 TKKIAHFDLKPENIMLLDKNIPPIPHIKLIDFGLAHEIDGVEFKNIFGTPPEVAPEIYN 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 309 KNOIYVHLDKPEKILKARN--SNELKIIDFGLARLDPKKSVKLFGTPPECAPEVNVY 366
OY 180 EPLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDFEEFHSHTSELAKDF 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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DB 367 QPVGLSTDMMTVGIVSYLLSGLSPLGDSDEDTLANVSASDMDFDDPSMDVYSDLAKDF 426
OY 240 IRKLLVKEETKRLTIQALRHPWI 263
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 427 ICRLIMIKDKRRKMSVODALRHPWI 450

```

RESULT 15

```

US-60-443-566-2540
; Sequence 2540, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001447
; CURRENT APPLICATION NUMBER: US/60/443, 566
; CURRENT FILING DATE: 2003-01-30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2540
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-443-566-2540

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Query Match      47.5%; Score 638; DB 7; Length 414;
Best Local Similarity 46.0%; Pred. No. 1e-53;
Matches 122; Conservative 65; Mismatches 66; Indels 12; Gaps 6;

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OY 4 GEEIUGQFAIVKKCREKSTGLEVAAKFIKKRQSRASRGVSREREVSILROYLHNH 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 64 GRELGKGFAYVKKRCIKKDSKEFAAKFMRRK---RKGDCHREIHEIETAVL-ELAQD 117
OY 63 N-VITLHDVYENRQDVHILEVSGGELFD--FLAQKESLSEBEATSTIKOILDGVNLT 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 118 NPWYNLHEVETASEMLVLEFYAAGSEIFDQCAVDREAKRKNDVQRLMQLIEGVHFL 177
OY 119 HTKIAHFDLKPENIMLLDKNIPPIPHIKLIDFGLAHEIDGVEFKNIFGTPPEVAPEIYN 178
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 178 HTRDVVHLDKPQNLITSES-PLGDIKIVDFGLSRILKNSSEELREIMGTPEYVAPEIIS 236
OY 179 YEPLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDFEEFHSHTSELAKD 238
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 237 YDPLSMATDMSIGVITYVMTLGTSPFLGNDKQETFLNISQMNLSYSEEDVLSESAYD 296
OY 239 FIRKLLVKEETKRLTIQALRHPWI 263
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 297 FIRTLVKKRPEDRATAEELKHPWL 321

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Search completed: March 26, 2003, 19:17:07
Job time : 24.6854 secs

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